

Fig 1.

SEQID22	MLLLGAVLLLLALPGHDQETTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID23	-----	
SEQID24	MLLLGAVLLLLALPGHDQETTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID25	MLLLGAVLLLLALPGHDQETTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID22	TPGEKGEKDPGLIGPKGDIGETGVPGAEGRGFPQIQGRKGEPEGAYVYRSAFSVGLE	120
SEQID23	-----MPGAEGPRGFPQIQGRKGEPEGAYVYRSAFSVGLE	36
SEQID24	TPGEKGEKDPGLIGPKGDIGETGVPGAEGRGFPQIQGRKGEPEGAYVYRSAFSVGLE	108
SEQID25	TPGEKGEKDPGLIGPKGDIGETGVPGAEGRGFPQIQGRKGEPEGAYVYRSAFSVGLE	120
SEQID22	TYVTIPNMPIRFTKIFYNQQNHYDGSTGFHCNIPGLYFFAYHITVYMKDVKVSLFKDK	180
SEQID23	TYVTIPNMPIRFTKIFYNQQNHYDGSTGFHCNIPGLYFFAYHITVYMKDVKVSLFKDK	96
SEQID24	-----	108
SEQID25	TYVTIPNMPIRFTKIFYNQQNHYDGSTGFHCNIPGLY-----	158
SEQID22	AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF	237
SEQID23	AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF	153
SEQID24	-----LLS-PTCPFALPRSSSTISKTTMMAP--LVNSTATFLGC	143
SEQID25	-----	158
SEQID22	LLYHDTN----- 244	
SEQID23	LLYHDTN----- 160	
SEQID24	T----T-LP-TTSQSI- 153	
SEQID25	-----LHRLSSLP 166	

Fig.2.

SEQID28	MLLQALLFLILPSHAEDDVTTTEELAPALVPPPCKTCAGWMAGIPGHPGHNTPGRDG	60
SEQID30	MLLQALLFLILPSHAEDDVTTTEELAPALVPPPCKTCAGWMAGIPGHPGH-----	52
SEQID29	MLLQALLFLILPSHAEDDVTTTEELAPALVPPPCKTCAGWMAGIPGHPGHNTPGRDG	60
SEQID26	MLLQALLFLILPSHAEDDVTTTEELAPALVPPPCKTCAGWMAGIPGHPGHNTPGRDG	60
SEQID27	-----	
SEQID28	---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPEAA---	AASL 113
SEQID30	-----	52
SEQID29	---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPEAAAY-----	110
SEQID26	RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPEAAAYMRSASFV	120
SEQID27	-----MTGAEGPRGFPGTPGRKGEPEAAAYVYRSASFV	33
SEQID28	-----	109
SEQID30	-----	52
SEQID29	-----	110
SEQID26	GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVL	180
SEQID27	GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVL	93
SEQID28	-----	FPMYP 118
SEQID30	-----IKIK-----FEGHP-----PG-----	63
SEQID29	-----	VYRSAFSVGLETRVTVP 129
SEQID26	KDKAVLFTYDQYQEKNVDQA-----SGSVLLHLEVGDQVWLQ-----	217
SEQID27	KDKAVLFTYDQYQEKNVDQA-----SGSVLLHLEVGDQVWLQ-----	130
SEQID28	FALLRSSTTNRIIMTAALASSTATFRDSTSLLTSRCT---	156
SEQID30	--RLNCAKIWHFLQD-----	76
SEQID29	NVPIRFTKIFYNQQN-HYDGSTGKFYCNIPGLYIYWLSSLP	169
SEQID26	--VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----	247
SEQID27	--VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----	160

Fig 3.

SEQID31	MPSPGTVCSSLGGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP----- 44
SEQID32	MPSPGTVCSSLGGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAP----- HVV 47
SEQID31	PAKLQPRALAGWLRPEDGGQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQD 104
SEQID32	PALPLSNQLCDLEQQRHAWASVFSQSTKDSCSDLTSGRTWGLRV----- 91
SEQID31	ILWEEAKEAPADK----- 117
SEQID32	LNRLFPPSSRERSRRSHQPSCSPEL 116

)

Fig 4.

SEQID33	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID38	-----MLQGKKVIVTGASKGIGREMAYHLAKMGAH	30
SEQID36	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID35	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID37	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID39	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID34	MAFMKKYLLPILGLFMAYYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAYHLAKMGAH	60
SEQID33	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	120
SEQID38	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	90
SEQID36	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	120
SEQID35	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	120
SEQID37	VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	102
SEQID39	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	120
SEQID34	VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLLILNH	102
SEQID33	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV	180
SEQID38	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV	150
SEQID36	ITNTSLNLFHDDIHHR-----PMLKQSNGSIVVVSSLAGKVAYPMV	162
SEQID35	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV	180
SEQID37	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV	162
SEQID39	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLA-----	172
SEQID34	ITNTSLNLFHDDIHHRKSMEVNFLSYVVLTVAAALPMLKQSNGSMCAL-----	150
SEQID33	AAYSASKFALDGFFSSIRKEYSVSRNVSVITLCVGLIDTETAMKAVSGIVHMQAAPKEE	240
SEQID38	AAYSASKFALDGFFSSIRKEYSVSRNVSVITLCVGLIDTETAMKAVSGIVHMQAAPKEE	210
SEQID36	AAYSASKFALDGFFSSIRKEYSVSRNVSVITLCVGLIDTETAMKAVSGIVHMQAAPKEE	222
SEQID35	AAYSASKFALDGFFSSIRKEYSVSRNVSVITLCVGLIDTETAMKAVSGIVHMQAAPKEE	240
SEQID37	AAYSASKFALDGFFSSIRKEYSVSRNVSVITLCVGLIDTETAMKAVSGIVHMQAAPKEE	222
SEQID39	-----ETAMKAVSGIVHMQAAPKEE	192
SEQID34	-----LLEYCYHVVHLSSX---	163
SEQID33	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	292
SEQID38	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	262
SEQID36	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	274
SEQID35	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	295
SEQID37	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	274
SEQID39	CALEIIKGGA LRQEEVYYDSSLWTTLLIRNPCR KILEFLYSTS YNMDRFINK---	244
SEQID34	-----	

Fig 5.

SEQID40	MAVMKNYLLPILVLFLAYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAHLSKMGAH	60
SEQID41	MAVMKNYLLPILVLFLAY-----	18
SEQID42	MAVMKNYLLPILVLFLAYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAHLSKMGAH	60
SEQID40	VVLTARSEEGLQKVVSRCLELGAAASAHYIAGTMEDMTFAEQFIVKAGKLMGGGLDMLILNH	120
SEQID41	YYYSTNEEFLQKVVSRCLELGAAASAHYIAGTMEDMTFAEQFIVKAGKLMGGGLDMLILNH	78
SEQID42	VVLTARSEEGLQKVVSRCLELGAAASAHYIAGTMEDMTFAEQFIVKAGKLMGGGLDMLILNH	120
SEQID40	ITQTSLSLFHDDIHSVRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI	180
SEQID41	ITQTSLSLFHDDIHSVRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMI	138
SEQID42	ITQTSLSLFHDDIHSVRVMEVNFLSYVVMSTAALPMLKQSNGSIAVISSLAGGRTVQQ	180
SEQID40	APYSASKFALDGFFSTIRTELYITKVNVSITLCVGLIDTETAMKEISGIINAQASPKEE	240
SEQID41	APYSASKFALDGFFSTIRTELYITKVNVSITLCVGLIDTETAMKEISGIINAQASPKEE	198
SEQID42	RSRSVTPDSRGP-----	192
SEQID40	CALEIIKGTLRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN	292
SEQID41	CALEIIKGTLRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN	250
SEQID42	-----	

Fig 6.

SEQID1	GTACCAGGAAAATAATGTGGACC	---	AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT	
SEQID2		-----	GTACTATCC-CCAACATGCCCATTC	
SEQID3	TT--CAG-----	TGTGGGATTGGAGACTTACGTACTATCC-CCAACATGCCCATTC		
SEQID4		*****	*****	*
SEQID1	GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGAAGGAGAGCGTAATGGACTCTATGCTG			
SEQID2	GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGAAGGAGAGCGTAATGGACTCTATGCTG			
SEQID3	GCTTTACCAAGATCTT-CTACA-----ATCAGAAAACCACTATGATGG-CTCCA--CTG			
SEQID4	GCTTTACCAAGATCTT-CTACA-----ATCAGAAAACCACTATGATGG-CTCCA--CTG			
SEQID1	ATAA-TGACAATG-----ACTCC-----AC-----			
SEQID2	ATAA-TGACAATG-----ACTCC-----AC-----			
SEQID3	GTAAATTCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACACATCACAGTCTATA			
SEQID4	GTAAATTCACTGCAACATTCCTGGGCTGTAC-----			
SEQID1	*****	*****	*****	*****
SEQID2				
SEQID3				
SEQID4				
SEQID1	-----			
SEQID2	-----			
SEQID3	AGTACCAGGAAAATAATGTGGACCAGGCCCTCGGCTCTGTGCTCCTGCATCTGGAGGTGG			
SEQID4	-----			
SEQID1	-----			
SEQID2	-----			
SEQID3	GCGACCAAGTCTGGCTCCAGGTGTATGGGAAGGAGAGCGTAATGGACTCTATGCTGATA			
SEQID4	-----			
SEQID1	-----			
SEQID2	-----			
SEQID3	ATGACAATGACTCCACCTCACAGGTTTCTTCTACCATGACACCAACTGA-----			
SEQID4	-----			
SEQID1	-----			
SEQID2	-----			
SEQID3	CTTCACAGGCTTTCTCTACCATGACACCAACTGATCACCAC			
SEQID4	-----			
SEQID1	-----			
SEQID2	-----			
SEQID3	CTTCACAGGCTTTCTCTACCATGACACCAACTGA-----			
SEQID4	-----			
SEQID1	-----			
SEQID2	-----			
SEQID3	*****	*****	*****	*****
SEQID4				
SEQID1	TAACTCAGAGCCTCCAGGCCAACAGCCCCAAAGTCATTAAAGGTTCAAGTACGG			
SEQID2	-----			
SEQID3	-----			
SEQID4	-----			
SEQID1	TTAGGAAGTTGATTATTAGTTAGTTGGAGGCCTTAGATATTATTCAATTACTCAT			
SEQID2	-----			
SEQID3	-----			
SEQID4	-----			

Fig 7.

SEQID5	ATGAGACCTGGCCACTTCTCCTCATTTCTGTCTGACGATTGTCAGTGGATCTGACGAC	60
SEQID6	-----GCTCATTCATCTTTAATTCA-----	21
SEQID7	ATGAGACCTGGCCACTTCTCCTCATTTCTGTCTGACGATTGTCAGTGGATCTGACGAC	60
SEQID8	-----	
SEQID9	-----	
SEQID5	ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCCTTAATCCTGCCAG	120
SEQID6	CCCATAAAGGCTTGGAAAACTAAGGCTGGAGATGAACCTAT-----AGGAGCCTGCCAGG	76
SEQID7	ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCCCTTAATCCTGCCAG	120
SEQID8	-----	
SEQID9	-----	
SEQID5	TCATGCCGAAGATGACGTTACTACAACGTGAAAGAGCTAGCTCCTGCTTGGCTCCACC	180
SEQID6	CCGTG-GAGAGTGGAGAACAGAGATGACGGAGATGATGTCTTCCCTGTCTGTGA--	132
SEQID7	TCATGCCGAAGATGACGTTACTACAACGTGAAAGAGCTAGCTCCTGCTTGGCTCCACC	180
SEQID8	-----	
SEQID9	-----	
SEQID5	CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC	240
SEQID6	-AATGGATTGGGGTAGA--GGTCCGGAGATAATGCCCTTGCTGGAAACAGT-----	183
SEQID7	CAAGGGAACTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC	240
SEQID8	-----	
SEQID9	-----	
SEQID5	ACCAGGCGGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG	300
SEQID6	-CTGGGCAGTTCTGTT---CCGCCATT-----ACAGAATTCTCTCATT---TCTAGG	232
SEQID7	ACCAGGCGGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG	300
SEQID8	-----	
SEQID9	-----	
SEQID5	TCTTCTTGGCTCTAACGGGTGAGACAGGGAGATGTTGGAATGACAGGGAGCTGAAGGGCACG	360
SEQID6	TCTTCTTGGCTCTAACGGGTGAGACAGGGAGATGTTGGAATGACAGGGAGCTGAAGGGCACG	292
SEQID7	TCTTCTTGGCTCTAACGGGTGAGACAGGGAGATGTTGGAATGACAGGGAGCTGAAGGGCACG	360
SEQID8	-----	
SEQID9	-----	
SEQID5	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAACGCCCTATGTGTATCG	420
SEQID6	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAACGCCCTATGTGTATCG	352
SEQID7	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAACGCCG-----	408
SEQID8	-----	
SEQID9	-----	
SEQID5	CTCAGCGTTCACTGTTGGGCTGGAGACCCCGTCACTGTTCCCAATGTACCCATTGCGTT	480
SEQID6	CTCAGCGTTCACTGTTGGGCTGGAGACCCCGTCACTGTTCCCAATGTACCCATTGCGTT	412
SEQID7	-----GTCACTGTTCCCAATGTACCCATTGCGTT	437
SEQID8	-----ATGAGACC--TGGCCACTTCTCCT	23
SEQID9	-----ATGAGACC--TGGCCACTTCTCCT	23
	*** * *** * * * * *** * * * *	
SEQID5	TACTAAAGATCTCTACAAACCAACAGAACTATTATGACGGCAGCACTGGCAAGTTCTACTG	540
SEQID6	TACTAAAGATCTCTACAAACCAACAGAACTATTATGACGGCAGCACTGGCAAGTTCTACTG	472
SEQID7	TACTAAAGATCTCTACAAACCAACAGAACTATTATGACGGCAGCACTGGCAAGTTCTACTG	497
SEQID8	CATTCTGTCTG-TACGATTGTCAG--TGAGATCTGACGCCACCAAAAG-GGCTCAGGATG	79
SEQID9	CATTCTGTCTG-TACGATTGTCAG--TGAGATCTGACGCCACCAAAAG-GGCTCAGGATG	79
	*** * *** * * * * *** * * * *	
SEQID5	CAACATTCCGGGACTCTACTACTTCTTACACATCACGGTGTACATGAAAGATGTGAA	600
SEQID6	CAACATTCCGGGACTCTACTACTTCTTACACATCACGGTGTACATGAAAGATGTGAA	532
SEQID7	CAACATTCCGGGACTCTACTACTTCTTACACATCACGGTGTACATGAAAGATGTGAA	557
SEQID8	CTACTGTTGCAAGCTCTCTGTTCTCTTAATCCTGCCAGT--CATGCCAAGATGAC	136
SEQID9	CTACTGTTGCAAGCTCTCTGTTCTCTTAATCCTGCCAGT--CATGCCAAGATGAC	136

SEQID5 ASTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAAAAAAA 1260
SEQID6 AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG----- 1184
SEQID7 AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG----- 1209
SEQID8 ACTCACTTGTTCATTAACGACTTTATAAAAATAATTGTGTTCTAGTCCAGAAAAAA 777
SEQID9 -----

SEQID5 AAAAAAAAAAGAAAAACTTTAGAGCACACTGGCGGCCGTTACTAG----- 1306
SEQID6 -----
SEQID7 -----
SEQID8 AGGCACACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATT 837
SEQID9 -----

SEQID5 -----
SEQID6 -----
SEQID7 -----
SEQID8 TGGTATGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTCT 897
SEQID9 -----

SEQID5 -----
SEQID6 -----
SEQID7 -----
SEQID8 GCTCACTGTACACAAATATTGTTCACATAAACCTATAATGAAATATGAAATACAGTGA 957
SEQID9 -----

SEQID5 -----
SEQID6 -----
SEQID7 -----
SEQID8 TTACTCTTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAG 1017
SEQID9 -----

SEQID5 -----
SEQID6 -----
SEQID7 -----
SEQID8 GGATAAATTGG 1028
SEQID9 -----

Fig 8.

SEQID10	ACTCTGGATGGGTGCTGTTAGACAAACGCCGTCTCCATATAAGACCTGACAGCACAGG	60
SEQID11	ACTCTGGATGGGTGCTGTTAGACAAACGCCGTCTCCATATAAGACCTGACAGCACAGG	60
	*****	*****
SEQID10	CACCACTCCGCCAGGACTGCAGGCCACCTGTCTGCACACCCAGCTGAGGCCATGCCCTCC	120
SEQID11	CACCACTCCGCCAGGACTGCAGGCCACCTGTCTGCACACCCAGCTGAGGCCATGCCCTCC	120
	*****	*****
SEQID10	CCAGGGACCGCTCTGCAGCCTCCTGCTCCGGCATGCTCTGGCTGGACTTGGCCATGGCA	180
SEQID11	CCAGGGACCGCTCTGCAGCCTCCTGCTCCGGCATGCTCTGGCTGGACTTGGCCATGGCA	180
	*****	*****
SEQID10	GGCTCCAGCTCCTGAGCCCTGAACACCAAGAGACTCAGCAGAGAAAGGAGTCGAAGAAAG	240
SEQID11	GGCTCCAGCTCCTGAGCCCTGAACACCAAGAGACTCAG--GTGAGACCTCCCCACAAAG	238
	*****	***
SEQID10	CCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGT	300
SEQID11	CCCCACATGTGTTCCAGGCCCTGCCACTTAGCAA-CCAGCTCTGT-----GACCT	287
	***	***
SEQID10	CAAGCAGAAGGGCAGAGGATGAACCTGGAAGTCCGGTCAACGCCCTTGTGATGTTGGA	360
SEQID11	GGAGCAGCAGGCCATCTC-TGGGCTTC-GTCTCTCCAGAGCACAAAGGACTCTGGG	345
	*****	***
SEQID10	ATCAAGCTGTCAGGGGTTCACTGACAGCACAGCC--AGGCCCTGGGAAGTTCTTC	418
SEQID11	TCTGACCT--CACTGTTCTGGAGGACATGGGGCTTAGAGCTCTAAACAGACTGTTTC	403
	***	***
SEQID10	AGGACATCCTCTGGGAAGAG-GCCAAAGAGGCCAGCCGACAAAGTGTGATGCCCAAGC	477
SEQID11	CCCCCTCCAGCAGAGAAAGGAGTCGAAGAACCC-ACCAGCCAAGCTGCAGCCC-CGAGC	460
	*	***
SEQID10	CTTACTCACCTCTCTAAAGTTAGAAGCGCTCATCTGGTTTCGCTTGCTGCAGC	537
SEQID11	TCTAGCAGGCTGGCTCC--GCCCGGAAGA-----TGG-----GCTCAAGCAGA	502
	**	***
SEQID10	AACTCCCACGACTGTTGACAAGCTCAGGAGGCGAATAAATGTCACAAACTGTATGCTGAT	597
SEQID11	AGGGGCAGAGGATGAACCTGGAAGTCCGGG--TCGGTACCTCTGCAG-TTTATGCTTCT	558
	*	***
SEQID10	GTTCCAAATGGGAATTATTCAAAGAGGAAAAGTTAATTTACTTTAAAAAAATCAA	657
SEQID11	GTGGCAGCAGGAGGGTGGGG-----	579
	**	***
SEQID10	AATAATAC 665	
SEQID11	-----	

Fig 9.

SEQID14	CTGCTTAGGAGGTTGTAGAAAGCTCG--TAGGTTCTCTGTGTCTACAGGAGTCT	119
SEQID18	CTGCTTAGGAGGTTGTAGAAAGCTCG--TAGGTTCTCTGTGTCTACAGGAGTCT	119
SEQID13	CTGCTTAGGAGGTTGTAGAAAGCTCG--TAGGTTCTCTGTGTCTACAGGAGTCT	119
***	***	*****
SEQID15	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
SEQID17	GAAACCGCAAGGAAGAGAGATGAAACAGAAGGAAAGCAGAGGAGGAGAGAGA	535
SEQID16	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
SEQID12	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
SEQID14	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
SEQID18	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
SEQID13	TCAG--GCCAGCTCCGTGGATGGCTTTATGAAAAAATATCCTCCCCATTCTGGG	177
***	***	*
SEQID15	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
SEQID17	GAGAAGAGAAGAAAAAGAAAAAGAACATCAATAAAAGAGTCAGATTGTTCGAAATC	595
SEQID16	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
SEQID12	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
SEQID14	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
SEQID18	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
SEQID13	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTAGACCC-----	225
***	***	*
SEQID15	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID17	TTGAGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	655
SEQID16	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID12	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID14	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID18	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID13	---AGAGATGCTCCAAGGAAAGAAAGTGTATTGTCACAGGGGCCAGCAAAGGGATCGGAAG	282
*****	*****	*****
SEQID15	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	342
SEQID17	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	715
SEQID16	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	336
SEQID12	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	342
SEQID14	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	342
SEQID18	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	342
SEQID13	AGAGATGGCTTATCATCTGGCAAGATGGGAGCCCAGTGGTGTGACAGCGAGGTCAA	336
*****	*****	*****
SEQID15	AGAAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTGGAGCAGCCTCAGCACACTA	402
SEQID17	AGAAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTGGAGCAGCCTCAGCACACTA	775
SEQID16	-----CTCAGCACACTA	348
SEQID12	AGAAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTGGAGCAGCCTCAGCACACTA	402
SEQID14	AGAAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTGGAGCAGCCTCAGCACACTA	402
SEQID18	AGAAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTGGAGCAGCCTCAGCACACTA	402
SEQID13	-----CTCAGCACACTA	348
*****	*****	*****
SEQID15	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	462
SEQID17	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	835
SEQID16	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	408
SEQID12	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	462
SEQID14	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	462
SEQID18	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	462
SEQID13	CATTGCTGGCACCATGGAAGACATGACCTTCGAGAGCAATTGTTGCCCCAACAGGAAA	408
*****	*****	*****
SEQID15	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	522
SEQID17	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	895
SEQID16	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	468
SEQID12	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	522
SEQID14	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	522
SEQID18	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	522
SEQID13	GCTCATGGGAGGACTAGACATGCTATTCTAACCCACATCACCACACTTCTTGAATCT	468
*****	*****	*****
SEQID15	TTTCATGATGATATTCAACCATGCGCGC-----	550
SEQID17	TTTCATGATGATATTCAACCATGCGCAAAAGCATGGAAGTCACATTCTCTAGTTACGT	955
SEQID16	TTTCATGATGATATTCAACCATGCGCAAAAGCATGGAAGTCACATTCTCTAGTTACGT	528

SEQID12 TTTTCATGATGATATTCAACCATGTGCGAAAGCATGGAAGTCACCTCTCAGTTACGT 582
 SEQID14 TTTTCATGATGATATTCAACCATGTGCGAAAGCATGGAAGTCACCTCTCAGTTACGT 582
 SEQID18 TTTTCATGATGATATTCAACCATGTGCGAAAGCATGGAAGTCACCTCTCAGTTACGT 582
 SEQID13 *****

SEQID15 -----CCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
 SEQID17 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 1015
 SEQID16 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
 SEQID12 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
 SEQID14 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
 SEQID18 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
 SEQID13 GGTCCCTGACTGTAGCTGCCTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 581

SEQID15 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 647
 SEQID17 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 1074
 SEQID16 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 647
 SEQID12 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 701
 SEQID14 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 701
 SEQID18 CTCCTCTGGCTGGAAAGTGGCTTATCCAAATGGTTGTCGC-TATTCTGCAAGCAAGT 656
 SEQID13 GCGCTCTCTGGCTGGAA-----TGCTATCATGTTGTCATCTGAGC 622

SEQID15 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 707
 SEQID17 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 1134
 SEQID16 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 707
 SEQID12 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 761
 SEQID14 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 761
 SEQID18 TTGCTTTGGATGGGTTCTTCTCCATCAGAAAGGAATTACAGTGTCCAGGGTCATG 761
 SEQID13 A-GTNGTTGATGG-----TCTCTCTCAT---AGAAGATATCAGG-----CAGGCATGATA 668

SEQID15 TATCAATCACTCTGTGTTCTGGCCTCATAGACACAGAACAGCCATG-AAGGCAGTT 766
 SEQID17 TATCAATCACTCTGTGTTCTGGCCTCATAGACACAGAACAGCCATG-AAGGCAGTT 1193
 SEQID16 TATCAATCACTCTGTGTTCTGGCCTCATAGACACAGAACAGCCATG-AAGGCAGTT 766
 SEQID12 TATCAATCACTCTGTGTTCTGGCCTCATAGACACAGAACAGCCATG-AAGGCAGTT 820
 SEQID14 TATCAATCACTCTGTGTTCTGGCCTCATAGACACAGAACAGCCATG-AAGGCAGTT 820
 SEQID18 -----AACACGCATG-AAGGCAGTT 676
 SEQID13 TACT-----TTGGTCTGCTATACCAAGACGCTAGGGCTCTGATGCA--- 708
 *** * * * ***

SEQID15 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
 SEQID17 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 1253
 SEQID16 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
 SEQID12 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
 SEQID14 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
 SEQID18 TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 736
 SEQID13 -----

SEQID15 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 886
 SEQID17 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 1313
 SEQID16 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 886
 SEQID12 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 940
 SEQID14 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 940
 SEQID18 GGGGGAGCTCGGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTCTG 796
 SEQID13 -----

SEQID15 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGAC 946
 SEQID17 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGAC 1373
 SEQID16 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGAC 946
 SEQID12 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGAC 1000
 SEQID14 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGGA- 999
 SEQID18 ATCAGAAATCCATGCAGGAAGATCCTGGAATTCTACTCAACGAGCTATAATATGGAC 856
 SEQID13 -----

SEQID15 AGATTCAAAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTGGGACTG 1006
 SEQID17 AGATTCAAAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTGGGACTG 1433

SEQID16 AGATTCAAAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTTGGGACTG 1006
 SEQID12 AGATTCAAAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTTGGGACTG 1060
 SEQID14 -----GGGACTG 1006
 SEQID18 AGATTCAAAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTTGGGACTG 916
 SEQID13 -----

 SEQID15 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 1066
 SEQID17 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 1493
 SEQID16 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 1066
 SEQID12 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 1120
 SEQID14 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 1066
 SEQID18 TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTCCAGAGTGTCCCCAG 976
 SEQID13 -----

 SEQID15 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1126
 SEQID17 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1553
 SEQID16 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1126
 SEQID12 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1180
 SEQID14 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1126
 SEQID18 AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTCCCTCTAACATTGCAAA 1036
 SEQID13 -----

 SEQID15 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1186
 SEQID17 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1613
 SEQID16 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1186
 SEQID12 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1240
 SEQID14 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1186
 SEQID18 ATGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAATTGTT 1096
 SEQID13 -----

 SEQID15 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1246
 SEQID17 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1673
 SEQID16 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1246
 SEQID12 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1300
 SEQID14 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1246
 SEQID18 ACTAAACATAGGTATAATTACCAAGATAGTTATTTAAATTATCTTATATATAATAAT 1156
 SEQID13 -----

 SEQID15 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1306
 SEQID17 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1733
 SEQID16 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1306
 SEQID12 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1360
 SEQID14 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1306
 SEQID18 ATGTGATGATTAATACAATATTAAATTATAATAAAGGTACATAAACTTTATAAATTCTA 1216
 SEQID13 -----

 SEQID15 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1366
 SEQID17 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1793
 SEQID16 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1366
 SEQID12 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1420
 SEQID14 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1366
 SEQID18 ACTGGTAGCTATAACTTGAGCTTATTCAAGGATGGTTCTTAAACCATAAACTGTACAA 1276
 SEQID13 -----

 SEQID15 ATGAAATTTTCAATATTGTTCTTAT 1394
 SEQID17 ATGAAATTTTCAATATTGTTCTTAT 1821
 SEQID16 ATGAAATTTTCAATATTGTTCTTAT 1394
 SEQID12 ATGAAATTTTCAATATTGTTCTTAT 1448
 SEQID14 ATGAAATTTTCAATATTGTTCTTAT 1394
 SEQID18 ATGAAATTTTCAATATTGTTCTTAT 1304
 SEQID13 -----

Fig 10.

SEQID19	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID20	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID21	*****	*****
SEQID19	GGTTTCTCGTGTCTACAGGGCAGGCTGAGCCAGGTCCCTGTTGATGGCAGTTAT	120
SEQID20	GGTTTCTCGTGTCTACAGGGCAGGCTGAGCCAGGTCCCTGTTGATGGCAGTTAT	120
SEQID21	GGTTTCTCGTGTCTACAGGGCAGGCTGAGCCAGGTCCCTGTTGATGGCAGTTAT	120
SEQID19	*****	*****
SEQID20	GAAAAATTACCTCTCCGATCTGGTGTCTTCCTGGCTACTACTACTATTCTACAAA	180
SEQID21	GAAAAATTACCTCTCCGATCTGGTGTCTTCCTGGCTACTACTACTATTCTACAAA	180
SEQID19	GAAAAATTACCTCTCCGATCTGGTGTCTTCCTGGCTACTACTACTATTCTACAAA	180
SEQID20	*****	*****
SEQID21	TGAAGAGTTCAAGACCAGAAATGCTCCAGGGAAAGAAAGTATTGTCAGTGGGCCAGCAA	240
SEQID19	TGAAGAGTTCAAGAC-----	194
SEQID20	TGAAGAGTTCAAGACCAGAAATGCTCCAGGGAAAGAAAGTATTGTCAGTGGGCCAGCAA	240
SEQID21	*****	*****
SEQID19	AGGGATTGGAAGAGAAATGGCATATCATCTGCAAAATGGGAGCCATGTGGTATTGAC	300
SEQID20	-----	-----
SEQID21	AGGGATTGGAAGAGAAATGGCATATCATCTGCAAAATGGGAGCCATGTGGTATTGAC	300
SEQID19	TGCCAGGTGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	360
SEQID20	-----TCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	234
SEQID21	TGCCAGGTGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	360
SEQID19	*****	*****
SEQID20	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTATTGT	420
SEQID21	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTATTGT	294
SEQID19	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTATTGT	420
SEQID20	*****	*****
SEQID21	*****	*****
SEQID19	CAAGGCGGGAAAGCTCATGGCGGACTGGACATGCTTATTCTAAACACATCACTCAGAC	480
SEQID20	CAAGGCGGGAAAGCTCATGGCGGACTGGACATGCTTATTCTAAACACATCACTCAGAC	354
SEQID21	CAAGGCGGGAAAGCTCATGGCGGACTGGACATGCTTATTCTAAACACATCACTCAGAC	480
SEQID19	*****	*****
SEQID20	CTCGCTGTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540
SEQID21	CTCGCTGTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	414
SEQID19	CTCGCTGTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540
SEQID20	*****	*****
SEQID21	*****	*****
SEQID19	CCTCAGCTACGGTGTGACGACAGCCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600
SEQID20	CCTCAGCTACGGTGTGACGACAGCCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	474
SEQID21	CCTCAGCTACGGTGTGACGACAGCCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600
SEQID19	*****	*****
SEQID20	CATTGCCGTACATCTCCTCTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	660
SEQID21	CATTGCCGTACATCTCCTCTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	534
SEQID19	CATTGCCGTACATCTCCTCTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	656
SEQID20	*****	*****
SEQID21	*****	*****
SEQID19	TGCAAGCAAGTTGCTCTGGATGGGTTCTTTCACCATAGAACAGAACTCTACATAAC	720
SEQID20	TGCAAGCAAGTTGCTCTGGATGGGTTCTTTCACCATAGAACAGAACTCTACATAAC	594
SEQID21	-----GCAGTGTACTCTGAC-----TCCCGC-----GGCCCGTATTAAATACAC	698
SEQID19	*****	*****
SEQID20	*****	*****
SEQID21	*****	*****
SEQID19	CAAGGTCAACGTGTCATCACTCTGTCCTGGCCTCATAGACACAGAAACAGCTAT	780
SEQID20	CAAGGTCAACGTGTCATCACTCTGTCCTGGCCTCATAGACACAGAAACAGCTAT	654
SEQID21	CAGCCACAGAACATGGAC-TGAAACCTGTATC---GATCTGGGGATTGGATATAACGAA	754
SEQID19	***	***
SEQID20	***	***
SEQID21	***	***
SEQID19	GAAGGAA--ATCTCTGGGATAATTAACGCCAACGCTTCTCCAAAGGAGGAGTGCGCCCTG	838
SEQID20	GAAGGAA--ATCTCTGGGATAATTAACGCCAACGCTTCTCCAAAGGAGGAGTGCGCCCTG	712
SEQID21	CATAGAATTACTCTGAGACTACCAGAACATGAA---TAGTTCAAATCAAATCATGCC---	808

